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## (57) Abstract

Use of the 5'-leader sequence of an RNA virus up to the first initiation codon of the viral RNA (or a derivative or portion thereof), either as RNA or a complementary DNA, as an enhancer of translation of mRNA when the 5'-leader RNA is contiguous with the mRNA.

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Translation of mRNA

This invention relates to enhancers of the translation of mRNA.

The mechanisms by which eukaryotes and prokaryotes initiate translation are known to have certain features in common and to differ in others. Eukaryotic messages are functionally monocistronic, translation initiates at the 5' end and is stimulated by the presence of a cap structure ( $m^7G5'ppp5'G\dots$ ) at this end (Shatkin, Cell 9 645 (1976)). Prokaryotic messages can be polycistronic, can initiate at sites other than the 5' terminus, and the presence of a cap does not lead to translational stimulation. Both eukaryotes and prokaryotes begin translation at the codon AUG, although prokaryotes can also use GUG. Translation in both is stimulated by certain sequences near the start codon. For prokaryotes, it is the so-called Shine-Dalgarno sequence (a purine rich region 3-10 nucleotides upstream from the initiation codon). For eukaryotes, it is a purine at the -3 position and a G residue in the +4 position (where the A of the AUG start codon is designated +1), plus other sequence requirements involved in finer tuning. This is part of the "relaxed" version of the scanning model (Kozak, Nuc. Acids. Res. 12, 857 (1984)) whereby a 40S ribosomal sub-unit binds at the 5' end of the eukaryotic mRNA and proceeds to scan the sequence until the first AUG, which meets the requirements of

the model, is encountered, at which point a 60S sub-unit joins the 40S sub-unit, eventually resulting in protein synthesis. Reference can be made in this connection to the following publications by Kozak : Cell 15, 1109 (1978), Nuc. Acid. Res. 9, 5233 (1981) and Cell 44, 283 (1986).

Beyond these sequence requirements in and about the initiation codon, there are no additional regions of mRNA which are known to enhance translation reproducibly.

During, eukaryotic transcription, sequences known as "enhancer" regions can provide transcriptional stimulation.

RNA viruses contain either positive or negative single-stranded RNA or double-stranded RNA. The class of RNA viruses include the majority of plant viruses (over 90%), some animal viruses and several bacteriophage.

One of the most widely studied of RNA viruses is tobacco mosaic virus (referred to hereinafter as TMV). The complete nucleotide sequence of TMV is known (Goelet et al., Proc. Natl. Acad. Sci. USA 79 5818 (1982)). The 5'- region of TMV RNA was first isolated in 1965 as an RNase T<sub>1</sub>-resistant fragment 70 nucleotides long (Mundry, Z. Vererbungsl. 97, 281 (1965)) and free of internal G residues (Mandeles, J. Biol. Chem. 243, 3671). This region (later referred to as omega, Mandeles J. Mol. Biol. Chem. 243 3671) was sequenced (Richards et al. Eur. J. Biochem. 84 513 (1978)) and shown to form disome initiation complexes with wheat germ ribosomes. One ribosome occupies the AUG initiation site of the 126 KDa

protein coding region and the second binds to the upstream leader sequence (Filipowicz and Haenni, Proc. Natl. Acad. Sci. USA 76, 3111 (1979); Konarska et al., Eur. J. Biochem. 114, 221 (1981)). Recent additional evidence to support the role of omega in ribosome association comes from the uncoating/gene expression data of Wilson and co-workers, (reviewed in J. Gen. Virol. 66, 1201 (1985) and UCLA Symp. 54 159 (1987)). It was observed in various in vitro translation systems that TMV particles are uncoated by the binding of ribosomes to the 5' end and their translational movement toward the 3' terminus.

It has now been found that the 5' - regions of RNA viruses act as enhancers of translation of mRNA.

According to a first aspect the present invention provides mRNA including the 5'- leader sequence of an RNA virus up to the first initiation codon of the viral RNA (or a derivative or portion thereof), the mRNA also including downstream sequence not derived from the virus providing the leader sequence.

According to a second aspect the invention provides a DNA sequence complementary to the 5'- leader sequence of an RNA virus, up to the first initiation codon of the viral RNA (or a derivative or portion thereof).

According to a third aspect the invention provides a DNA sequence comprising a promoter, a sequence complementary to the 5'- leader sequence of an RNA virus up to the first

initiation codon of the viral RNA (or a derivative or portion thereof) and an open reading frame including an appropriate initiation codon. The invention also provides an expression vector including such a DNA sequence.

According to a fourth aspect the invention provides the use of the 5'- leader sequence of an RNA virus up to the first initiation codon of the viral RNA (or a derivative or portion thereof), either as RNA or as complementary DNA, as an enhancer of translation of mRNA when the 5'- leader RNA is contiguous with the mRNA.

Most RNA viruses which have been sequenced contain 5'- leader sequences, i.e. sequences at the 5'- end up to but not including the first initiation codon. Appropriate 5'- leader sequences from any RNA virus may be used as a translational enhancer according to the invention.

As noted above, the 5'- leader sequence of TMV plus the AUG initiation codon is known as omega and its nucleotide sequence is known (Richards *et al.* Eur. J. Biochem. 84, 513 (1978)) so that cDNA can be prepared synthetically. The omega prime ( $\Omega'$ , see Figure 1) sequence of TMV represents the preferred translational enhancer according to the invention.

Information is also available about the translational enhancement by 5'- leader sequences of other RNA viruses including the following:

Turnip yellow mosaic virus genome RNA (Filipowicz and Haenni, Proc. Natl. Acad. Sci. USA 76 3111 (1979)), bromo

mosaic virus RNA 3, alfalfa mosaic virus RNA 4 (Goelet et al., Proc. Natl. Acad. Sci. USA 79 5818 (1982)); Rous Sarcoma virus (J.L. Darlix et al. Nuc. Acids Res. 10, 5183 (1982)).

In any particular case it will almost certainly be possible to vary the natural 5'- leader sequence in such a way that its function as a translational enhancer is modulated but not destroyed. Such variants are referred to herein as "derivatives" and derivatives of the natural sequence and their use as translational enhancers form part of the present invention. It may also be the case that parts only of the natural 5'- leader sequence (or a derivative sequence) are required to provide translational enhancement. Such parts of the sequence are referred to herein as "portions" and portions of the natural sequence or of derivatives thereof and their use as translational enhancers form part of the present invention.

In any particular case, determination of the nucleotide sequence of the 5'- leader of an RNA virus should be within the expertise of a man of ordinary skill in the art using known and readily available techniques. Similarly, identification of those parts of the natural 5'- leader sequence which are essential for translational enhancement and those which can be modified or omitted (i.e. the identification of derivatives and portions of the natural sequence) is a matter which can be determined by routine experimentation.

The 5'- leader sequences of RNA viruses (or derivatives or portions thereof) can be used as such as translational enhancers according to the invention by ligating them upstream of an appropriate mRNA using for example T<sub>4</sub> RNA ligase. The 5'- leader sequence may be immediately adjacent to the initiation codon of the downstream mRNA, or it may be spaced therefrom by an intervening sequence. However, it is preferred to use the 5'- leader sequence in the form of complementary DNA. The cDNA can be obtained in any manner which is desired. However in view of the relatively short length of the 5'- leader sequences in question it will usually be most convenient to synthesise the cDNA chemically. The cDNA will generally be incorporated into an expression vector. An expression vector is any vector capable of expressing those DNA sequences contained therein which are operably linked to other sequences capable of effecting their expression. An expression vector will usually contain a DNA sequence comprising a promoter, the sequence complementary to the 5'- leader sequence of an RNA virus up to but not including the first initiation codon of the viral RNA (or a derivative or portion thereof) and an open reading frame including an appropriate initiation codon. The open reading frame will generally code for one or more proteins of interest. The expression vector may be introduced directly into the host cell stably or transiently where the DNA sequence is expressed by transcription and translation. In

the case of stable expression the vector must be replicable in the host either as an episome or as an integral part of the chromosomal DNA. Alternatively the expression vector can be transcribed in vitro and the RNA introduced directly into the cell for transient expression.

The translational enhancers according to the invention can be used in any situation where it is desired to enhance the translational efficiency of mRNA. However it should be noted that the effect of the enhancers is most marked in the case of an mRNA which is otherwise poorly translated. Thus the addition of either a cap or an enhancer according to the invention or both will stimulate translation. In the case of an mRNA already bearing a cap the effect of the enhancer according to the invention, is still present.

The translational enhancers according to the invention are effective in many different types of expression system, for example plant cells, bacteria and animal cells although a particular enhancer may be more suitable for one system rather than another. For example during testing in vitro the omega sequence of TMV appears to show a greater degree of enhancement in the wheat germ system and E. coli than in the rabbit reticulocyte lysate system although enhancement of translation is observed in all three systems. The matching of particular enhancers to particular expression systems will generally be a matter well within the expertise of the man of ordinary skill.

In general the translational enhancers according to the invention can be used with advantage in any case where the value of an organism or cell line to commerce, including agriculture, is determined by the level of expression of one of its natural genes or of an artificially introduced gene.

(i) In the manufacture of commercially useful proteins in genetically engineered organisms or cell lines.

(ii) In fermentation where the rate of production of a product of intermediary metabolism catalysed by enzymes can be enhanced by increasing the rate of synthesis of a particular enzyme.

(iii) In viral cross-protection where the effects of a viral infection can be reduced by prior exposure to an attenuated form of the virus and it is advantageous to increase the level of protection by increasing the level of production of the component which provides the protection. For example plants can be protected against infection by TMV by exposing them to a genetically engineered strain of Agrobacterium which contains a cDNA copy of that portion of the TMV RNA which codes for the viral coat protein. Bacterial cDNA inserted in the plant genome continually expresses the coat protein which protects the plant against infection by the virus itself.

(iv) In the genetic engineering of plants where a property such as herbicide resistance is installed by artificial modification of the intermediary metabolism of the

plant.

(v) In the expression of a partial clone of a gene, for example where it is desired to raise antibodies to the product of expression of the partial clone.

The invention is illustrated further by the following experimental work.

#### EXPERIMENTAL

##### mRNA

Chimaeric mRNA according to an embodiment of the invention was produced in the following manner, as illustrated in Figure 1.

Using the sequence of TMV RNA vulgare strain (Goelet *et al.*, Proc. Natl. Acad. Sci. USA 79 5818 (1982)), an 81 base oligonucleotide was synthesised containing the DNA sequence complementary to the 67 base sequence upstream of the AUG initiation codon of the 126 kDa open reading frame, but not including the 5' cap ( $\text{m}^7\text{Gppp}$  and adjacent G residue). This sequence is called omega prime. A HindIII site was incorporated at the 5' end and a Sal I site at the 3' end of this oligonucleotide. A second oligonucleotide of 20 bases, including 13 bases at the 3' end of the omega prime sequence and a Sal I site, was synthesized as a primer for the synthesis of the second strand. After annealing, second strand synthesis was completed using the Klenow fragment of DNA polymerase I.

The resulting double-stranded 81 bp fragment was

digested with HindIII/Sal I to create a 79 bp fragment with single-stranded cohesive ends and inserted into the corresponding sites of pUC19. The fact that the synthesis had resulted in the correct orientation of the omega prime sequence of TMV was verified by sequence analysis using the dideoxy chain termination method (Sanger *et al.*, Proc. Natl. Acad. Sci. USA 74, 5463 (1977)). The fragment containing omega prime of TMV was then introduced into the HindIII/Sal I sites of plasmid pJIII to result in pJIII101. pJIII is derived by inserting the TMV origin of assembly sequence as a BamHI fragment into the corresponding site of pSP64 (Melton, Nuc. Acids Res. 12 7035 (1984)) and modifying the SmaI site to a Bgl II site (Sleat *et al.* Virology 155, 299 (1986)).

A 779 bp Sal I ended fragment from pCML (Close and Rodriguez, Gene 20, 305 (1982)) containing the chloramphenicol acetyltransferase gene (CAT) of Tn9 was introduced into the Sal I site of pJIII and pJIII101, resulting in pJII2 and pJII102, respectively. A 1.2 kb Bgl II/Sal I fragment from pKNR-H (Gallie *et al.*, J. Bacteriol. 161, 1034 (1985)) containing the neomycin phosphotransferase II gene (NPTII) of Tn5 was made blunt ended with Klenow fragment and introduced into the Acc I site of pJIII and pJIII101 to result in pJII3 and pJII103, respectively. Correct orientation of both the CAT and NPTII genes was verified by restriction fragment analysis.

After linearisation of pJII2 and pJII102 with Bgl II and

pJII3 and pJII103 with EcoRI, RNA transcripts of each were made using SP6 RNA polymeras . Capped versions of each were also made using GpppG and SP6 polymerase reaction conditions which ensure comparable yields of capped transcripts. Equivalent yields of RNA from the capped and uncapped reactions and for the constructs with or without the omega sequence were verified by denaturing formaldehyde-agarose gels.

Equivalent amounts of the various CAT containing transcripts and the NPTII containing transcripts were added to the rabbit reticulocyte lysate (MDL), wheat germ S-30 (WG) and E. coli S-30 in vitro translation systems under standard reaction conditions. The resulting polypeptide products were labelled with <sup>35</sup>S-methionine.

Figures 2 and 3 show the SDS-PAGE analysis of the translation products from MDL (Fig. 2, tracks 1 to 11), WG (Fig. 2, tracks 12 to 22) and E. coli (Fig. 3). In Figure 2 template additions were: tracks 1 and 12, H<sub>2</sub>O (endogenous translation); tracks 2 and 13, BglII-linearized pJII102 DNA; tracks 3 and 14, CAT RNA; tracks 4 and 15, omega prime-CAT RNA; tracks 5 and 16, 5'-capped CAT RNA; tracks 6 and 17, 5'-capped-omega prime-CAT RNA; tracks 7 and 18, EcoRI-linearized pJII103 DNA; tracks 8 and 19, NPTII RNA; tracks 9 and 20, omega prime-NPTII RNA; tracks 10 and 21, 5'-capped NPTII RNA; tracks 11 and 22, 5'-capped-omega prime-NPTII RNA. <sup>14</sup>C-labelled marker proteins (Amersham International, plc)

were loaded on track M. Their respective sizes in kilodaltons (kDa) are shown on the left. The dried gel was autoradiographed for 3 days at room temperature. In Figure 3 template additions were: track 1, H<sub>2</sub>O (endogenous translation); track 2, BglIII-linearized pJII102 DNA; track 3, CAT RNA; track 4, omega prime-CAT RNA; track 5, 5'-capped CAT RNA; track 6, 5'-capped-omega prime-CAT RNA; track 7, EcoRI-linearized pJII103 DNA; track 8, NPTII RNA; track 9, omega prime-NPTII RNA; track 10, 5'-capped NPTII RNA; track 11, 5'-capped-omega prime-NPTII RNA. <sup>14</sup>C-labelled marker proteins were loaded on track M and their sizes (in kDa) are shown on the left. The dried gel was autoradiographed for 3 days at room temperature. It should be noted that although the E. coli S-30 system is a transcriptionally active system, the native E. coli RNA polymerase does not recognise the SP6 promoter.

The following Table 1 shows the stimulating effect of the omega prime sequence. Zones from gels shown in Figures 2 and 3 were excised and the radioactivity in each band of product of translation was measured and the data normalised in each case to that from RNA not containing the omega prime sequence. Expressing the data in this way eliminates any stimulating effect of the cap alone and shows only the stimulating effect of the omega prime sequence.

Table I

mRNA	<u>WG</u>	<u>MDL</u>	<u>E. coli</u>
CAT	1	1	1
omega prime-CAT	10	1.2	11
GpppG-CAT	1	1	1
GpppG-omega prime-CAT	3.8	2.2	2.7
NPTII	1	1	1
omega prime-NPTII	71	17.8	74
GpppG-NPTII	1	1	1
GpppG-omega prime-NPTII	9.5	1.9	9.6

DISCUSSION

The presence of the omega prime region of TMV stimulates the expression of transcripts containing either the CAT or NPT II sequences in either the capped or uncapped state. Stimulation was most marked with the translationally inefficient NPTII transcripts. Thus, the Tn5 fragment containing the NPTII gene contains an additional AUG immediately upstream from the AUG start codon of the NPTII gene. In addition, the "Kozak rules" (see the papers by Kozak referred to above) would suggest that the region about the NPTII start codon constitutes a poor signal for translational initiation. As seen in WG and MDL (Figure 2, lanes 8 and 19), the NPTII transcript without either a cap or omega prime functions poorly. The addition of a cap or omega prime improves translation although the presence of omega prime has a greater stimulatory effect than the presence of a cap alone. E. coli translational machinery, although not cap-dependent, is greatly stimulated by the presence of the omega prime sequence (Figure 3, lanes 4, 6, 9 and 11). In E. coli, addition of a cap to the omega prime sequence on CAT or NPTII mRNA did little to enhance its translation whereas addition of omega prime to capped CAT or NPTII mRNA resulted in greater enhancement.

CAT gene mRNA, even without a cap or the omega prime sequence, functions more efficiently in the eukaryotic systems. The first AUG from the 5' terminus is the start

codon for CAT and the sequence in and about the start codon conforms well to the "Kozak rules". This is most evident in the MDL system where a much lower mRNA concentration was required to prevent exhaustion of the available  $^{35}\text{S}$ -methionine pool. Not surprisingly then, the presence of the omega prime sequence in CAT mRNA was less stimulatory. MDL is thought less cap-dependent than WG, however the presence of a cap on the NPTII transcript had a slight stimulatory effect (Figure 2, lanes 8 and 10), whereas its presence on the CAT transcript had little effect (Figure 2, lanes 3 and 5). CAT mRNA alone was much less active in the WG system. As a result, the presence of either a cap or the omega prime sequence or both was highly stimulatory (Figure 2, lanes 14 to 17). In WG, addition of a cap to the omega prime sequence on NPTII mRNA (Figure 2, lanes 20 and 22) did little to enhance its translation whereas addition of omega prime to capped or uncapped NPTII mRNA (Figure 2, lanes 19 and 21) resulted in a greater enhancement.

Therefore the presence of the omega prime sequence enhances translation in both eukaryotic (MDL and WG) and prokaryotic systems. This is consistent with the ability of TMV particles to be uncoated and the RNA translated by eukaryotic or prokaryotic translational machinery. The omega prime sequence often has a greater stimulatory effect on the expression of transcripts than does the presence of a cap alone. In addition, the omega prime sequence enhances

translation under conditions where capping does not, e.g. in the prokaryotic and, to some extent, the MDL systems.

#### FURTHER EXPERIMENTAL WORK

Chimaeric RNA constructs including CAT mRNA and derivatives or portions of the omega prime leader sequence were made in an analogous manner to that described above, the initial synthetic DNA sequence being chosen to produce the required RNA. As shown in Figure 4, there were five deletions (referred to as  $\Delta 1$  to  $\Delta 5$ ), one A  $\rightarrow$  C transversion and one  $[C,A]_n \rightarrow [U]_n$  substitution.

Further chimaeric RNA constructs containing CAT mRNA were made in an analogous manner with 5'-leader sequences of viruses other than TMV (U1, vulgare, or common strain), namely the tomato strain of TMV (SPS isolate), Turnip Yellow Mosaic Virus (TYMV), Brome Mosaic Virus RNA 3 (BMV 3), Rous Sarcoma Virus partial leader (RSV) and Alfalfa Mosaic Virus RNA 4 (AlMV4). The initial DNA sequences synthesised and restriction site diagrams are shown respectively in Figures 5 to 9.

A further set of RNA constructs was prepared in an analogous manner, but with the E.coli reporter gene  $\beta$ -glucuronidase (GUS) in place of CAT. The leader sequences used were either polylinker (for comparison purposes) or UI omega (i.e. omega prime from TMV) or the derivatives and portions of omega prime and other viral leaders as described above. The GUS gene was used either in an artificial "good"

Kozak context (see p. 33, re. Table 9) or in the native "bad" Kozak context as a SallI fragment from pRAJ235/240 (Jefferson et al. Proc. Natl. Acad. Sci. 83 8447 (1986)). The leader sequences and restriction site diagrams are shown in Figures 10 to 13. The expression of the reporter gene was determined fluorimetrically as described by Jefferson et al. Proc. Natl. Acad. Sci. 83 8447 (1986).

In addition to the three in vitro translation systems described above, two in vivo systems were used: microinjection of Xenopus laevis oocytes and electroporation of tobacco (Nicotiana Tabacum cv' Xanthi) mesophyll protoplasts. The respective techniques were as follows:

Two ng of each synthetic SP6 mRNA (or their corresponding DNA templates) were microinjected into the cytoplasm of stage 6 X. laevis oocytes in batches of 30 using standard procedures (Colman A. In Hames, B.D. and Higgins, S.J. (eds.), Transcription and Translation: A Practical Approach, IRL Press, Oxford. 271 (1984)). Oocytes were incubated for 18 hours in Modified Barths' Saline (MBS), then washed briefly in distilled water. Extracts from Xenopus oocytes were prepared by resuspending each sample in 0.25 M Tris-HCl, pH 7.4, containing 10 mM DTT (17  $\mu$ l/oocyte), followed by sonication for 15 sec. Insoluble material was removed by microcentrifugation for 15 min. and fractions of the resultant extract representing equivalent numbers of oocytes were assayed for CAT or GUS activity by published

procedures (CAT: Gallie *et al.* Nuc. Acids. Res. 15 3257 (1987); GUS: Jefferson *et al.* Proc. Natl. Acad. Sci. 83 8447 (1986)).

Mesophyll protoplasts were isolated from leaves of N. tabacum (cv. Xanthi) and stored in 0.7 M mannitol. The protoplasts ( $10^6$ ) were centrifuged at 60xg for 3 min, resuspended in 1 ml ice-cold 0.7 M mannitol containing the RNA ( $8\mu\text{g}$ ), transferred to the electroporation cell and given a single voltage pulse (2.5 kV/cm) by discharging a 50 nF capacitor through the cell. The pulse had a rapid rise-time (less than 1  $\mu\text{s}$ ) and an exponential decay with a half-life of about 5  $\mu\text{s}$ . Electroporated protoplasts were stored at 0-4°C for 10 min. Ten mls of 0.7 M mannitol were added and the protoplasts recovered by centrifugation at 60xg for 3 min. The protoplasts were then resuspended in culture medium and incubated at 25°C for 21 hours in 9 cm-diameter Petri dishes.

Each sample of electroporated protoplasts was sedimented, resuspended and sonicated in 150  $\mu\text{l}$  of 0.25 M Tris-HCl, pH 7.4 containing 2 mM leupeptin and 10 mM dithiothreitol (DTT) for CAT assays or 50mM sodium phosphate pH 7.0, 10mM 2-mercapto ethanol for GUS assays. Extracts were microcentrifuged at 10,000xg for 10 min at room temperature or 4°C.

Figure 14 shows the effect of omega prime on the expression of capped or uncapped CAT RNAs in electroporated tobacco protoplasts. Each origin spot received extract

equivalent to  $5 \times 10^4$  viable protoplasts. For each sample, the conversion (%) of substrate ( $^{14}\text{C}$ -chloramphenicol) into its mono-acetylated forms (indicated on the left) is shown at the top of the track. Electroporated RNAs or standards were: track 1, no RNA (mock); track 2, CAT RNA; track 3, omega prime-CAT RNA; track 4, 5'-capped CAT RNA; track 5, 5'-capped-omega prime-CAT RNA; track 6, 0.1 unit purified CAT enzyme added to an equivalent volume of extract as for track 1; track 7, 0.1 unit purified CAT enzyme alone. The dried tlc plate was autoradiographed for 2 days before removing and determining the radioactivity in the relevant  $^{14}\text{C}$ -labelled spots of mono-acetylated products (3-Ac/1-Ac), % conversion data reflects the relevant CAT activity in the extract. Omega prime (+/- a 5'-cap) was the most stimulatory of CAT RNA expression.

Figure 15 shows the effect of omega prime on the expression of capped or uncapped CAT RNAs microinjected into X. laevis oocytes. An equal amount of each CAT RNA-construct or linearized DNA template (2 ng) was injected per oocyte, throughout. Equal oocyte extract volume (equivalent to  $0.3 \times$  cell) were assayed in each case, unless stated otherwise. Conversion (%) of  $^{14}\text{C}$ -chloramphenicol into its mono-acetylated forms, is shown at the top of each track. In tracks 5 and 6, conversion (%) into the di-acetylated form is indicated by \*. Microinjected RNAs or standards were: track 1, no RNA (mock); track 2, BglIII-linearized pJIII102; track 3,

CAT RNA; track 4, omega prime-CAT RNA; track 5, 5'-capped CAT RNA; track 6, 5'-capped-omega prime-CAT RNA; track 7, as for track 5 but 20-fold diluted extract; track 8, as for track 6 but 20-fold diluted; track 9, 0.1 unit purified CAT enzyme added to an equivalent volume of extract as in track 1; track 10, 0.1 unit purified CAT enzyme alone. The dried tlc plate was autoradiographed at room temperature for 18 hours, before excising and counting the relevant  $^{14}\text{C}$ -labelled spots.

The following Tables show the further results obtained.

Table 2

Effect of deletions and other sequence alterations on translational enhancement by omega prime. Chloramphenicol acetyltransferase expression in RNA-microinjected Xenopus oocytes.

RNA injected	% conversion of $^{14}\text{C}$ -chloramphenicol to the 1- and 3-monoacetylated forms
Nil (mock)	0.1
CAT	4.5
Omega prime CAT	34.2
$\Delta 1$ - CAT	17.2
$\Delta 2$ - CAT	9.7
$\Delta 3$ - CAT	17.6
$\Delta 4$ - CAT	14.6
$\Delta 5$ - CAT	17.9
A -> C transversion - CAT	15.7
[C,A] <sub>n</sub> -> [U] <sub>n</sub> substitution - CAT	34.3
0.1 units CAT (pure enzyme)	1.2
All RNA's were uncapped	

The above results show that omega prime enhances translation of CAT. Deletions 1 to 5 reduce this effect without destroying it entirely. The same is true of the A -> C transversion. The [U]<sub>n</sub> substitution has little effect, if any.

Table 3

Effect of untranslated 5'-leader sequences from different viruses on the level of expression of chloramphenicol acetyltransferase after microinjection of mRNA into Xenopus oocytes.

RNA injected	% conversion of $^{14}\text{C}$ -chloramphenicol to the 1- and 3-monoacetylated forms
Nil (mock)	0.1
CAT	6.3
Omega U1 CAT	46.5
Omega (SPS) CAT	35.8
TYMV CAT	1.3
BMV3 CAT	5.0
RSV CAT	5.4
AlMV4	6.7
0.1 Units CAT (pure enzyme)	1.3

All RNAs were uncapped

Omega U1 derives from the standard strain of TMV (Vulgare).

Omega SPS is from the tomato strain of TMV.

TYMV: turnip yellow mosaic virus leader.

BMV3: brome mosaic virus RNA3.

RSV: a partial leader sequence from Rous Sarcoma virus.

AlMV4: alfalfa mosaic virus RNA4.

The above results show that omega prime from TMV U1 enhances translation of CAT RNA in this system. TMV tomato strain omega prime also does so, but a little less well. Other viral leaders have little or no effect, TYMV leader may be inhibitory.

Table 4

Effects of different 5'- non-translated leader sequences with or without a 5'-cap on in vitro translation of chloramphenicol acetyltransferase mRNA in a wheat germ cell-free system. (The results as shown below have been normalized to the unmodified CAT mRNA leader sequence which was taken as 1.0 to show fold-stimulation over CAT mRNA alone).

RNA added	Uncapped	capped
CAT	1.0	1.0
Omega prime CAT	2.8	3.7
Δ1-CAT	1.2	0.6
Δ2-CAT	2.0	1.8
Δ3-CAT	1.5	1.3
Δ4-CAT	3.0	1.5
Δ5-CAT	1.5	0.7
A -> C transversion-CAT	3.3	2.9
[C,A] <sub>n</sub> ->[U] <sub>n</sub> substitution-CAT	2.1	3.4
TMV Tomato strain Omega prime-CAT	1.7	3.0
TYMV-CAT	0.3	3.0
BMV3-CAT	1.4	2.8
RSV-CAT	0.6	2.5
AlMV4-CAT	2.1	2.3

Note: these figures represent comparisons of proportional stimulations of translation produced by the inclusion of different sequences at the 5' end of the CAT message. Translations were done with capped or with uncapped messages. Each column represents the yield of radioactive CAT protein recovered by excision from an independent gel (as in Figures 2 and 3). The bands were cut out, counted, and have been normalised to a band for which the mRNA was unmodified CAT message.

The above results show that omega prime enhances in this system, with or without 5'-capping. The other viral leader sequences and derivatives or portions of omega prime enhance translation to varying extents, but rarely significantly more than omega prime itself.

Table 5

Effects of different non-translated leader sequences, all without a 5'-cap structure, on in vitro translation of chloramphenicol acetyltransferase mRNA in an E. coli cell-free system.

RNA added	Uncapped
CAT	1.0
Omega prime CAT	9.0
$\Delta_1$ - CAT	3.3
$\Delta_2$ - CAT	2.5
$\Delta_3$ - CAT	6.3
$\Delta_4$ - CAT	4.2
$\Delta_5$ - CAT	3.8
A $\rightarrow$ C transversion CAT	4.1
[C,A] <sub>n</sub> $\rightarrow$ [U] <sub>n</sub> substitution CAT	1.9
TMV Tomato strain Omega CAT	6.6
TYMV CAT	0.2
BMV3 CAT	3.7
RSV CAT	1.5
A1MV4 CAT	1.4

The above results show that omega prime, some of its derivatives, and tomato strain omega prime enhance translation to the greatest extent. Most of the other sequences also enhance, but to varying extents. E. coli does not require a 5' cap for translation.

Table 6

Effect of different leaders on the translation of  $\beta$ -glucuronidase mRNA (from pRAJ235/240) electroporated into tobacco protoplasts.

GUS mRNA construct used *	nmoles 4-methyl umbelliferyl glucuronide cleaved min <sup>-1</sup> /μg protein in protoplast extract	Fold Stimulation
---------------------------	--	------------------

[Blank] (no mRNA)

Uncapped Leader

235 [SP6 transcript,

polylinker leader.]	<0.01	1
Omega prime (U1)-235	0.25	>25
Omega prime (SPS)-235	0.15	>15
TYMV -235	<0.01	-
A1MV4 -235	<0.01	-
BMV3 -235	<0.01	-
RSV -235	<0.01	-

Capped Leader

capped 235 [SP6

transcript polylinker

leader]	0.03	1
capped Omega prime -235	0.54	18

capped Omega prime

(SPS) -235	0.43	14
capped TYMV -235	<0.01	-
capped AlMV4 -235	0.23	8
capped BMV3 -235	0.23	8
capped RSV -235	0.21	7
capped $\Delta 1$ -235	0.55	18
capped $\Delta 2$ -235	0.50	17
capped $\Delta 3$ -235	0.32	11
capped $\Delta 4$ -235	0.54	18
capped $\Delta 5$ -235	0.54	18

capped A->G transversion

-235	0.69	23
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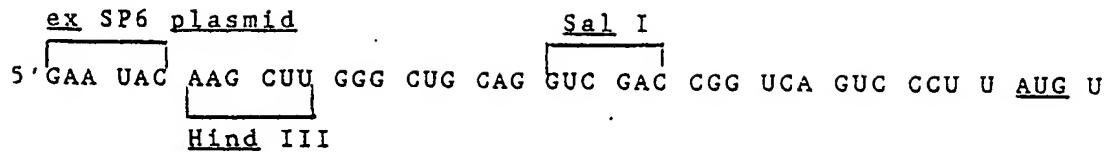
capped [C,A]<sub>n</sub>->[U]<sub>n</sub>

substitution <0.01 -  
 (blank value subtracted from all  
 others)

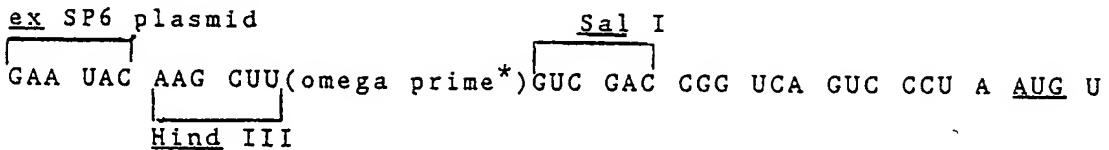
(\* Constructs were "bad" GUS ex pRAJ (235/240), with or without a 5' cap)

All mRNA constructs were electroporated at 8 $\mu$ g/ml and washed protoplasts incubated for 20 hours as described (Gallie et al Nuc. Acids. Res. 15, 3257 (1987)).

The sequence of the "Bad" Kozak construct (235) leader is as follows:



The insertion of Omega prime into the polylinker is as below:



\* wherein omega prime sequence is as below:-

UAU UUU UAC AAC AAU UAC CAA CAA CAA ACA ACA AAC AAC AUU  
ACA AUU ACU AUU UAC AUU UAC A

and the deleted omega prime derivatives, etc follow accordingly.

Messenger RNAs encoding calf preprochymosin or chicken prelysozyme were synthesized in vitro, with or without the TMV 5'-terminal sequence (omega prime). The mRNAs were translated in vitro in the systems derived from rabbit reticulocytes (MDL), wheat-germ (WG) or E. coli (EC).

The plasmids pJII6 and pJII7 (Figure 16) were constructed using components of plasmids pSP64CT and pSP64LT (Sleat et al. Virology, 155 299 (1986)) and pJII101. Both pJII6 and pJII7 are derivatives of the transcription plasmid pSP64 (Melton, 1984), which contains a promoter for the bacteriophage SP6 RNA polymerase adjacent to the polylinker sequence derived from M13 mp11. The preprochymosin and prelysozyme coding regions of pSP64CT and pSP64LT respectively were excised as HindIII fragments, blunt-ended

with the Klenow fragment of DNA polymerase 1, and cloned into the HincII site of pJIII01 to generate pJII6 and pJII7 respectively (Figure 16). These constructs were used to direct the synthesis of messenger-sense preprochymosin and prelysozyme transcripts bearing a 5'-terminal omega prime sequence. Parental plasmids pSP64CT and pSP64LT were templates for synthesis of mRNAs lacking omega prime.

The results are shown in Table 7 below.

Table 7

Effect of omega prime on expression of two eukaryotic mRNAs in 80S- and 70S-ribosome-based translation systems.

Incorporation of L-[<sup>35</sup>S]-methionine (cpm) into gel-purified polypeptides.

Cell-free system	CPM (Rel. Stimulation)		
	MDL	WG	<u>E. coli</u>
<b>SP6 transcript</b>			
Prelysozyme	5040 (1.0)	3730 (1.0)	0 (1.0)
omega prime prelysozyme	5290 (1.0)	10240 (2.8)	1030 ( )
Preprochymosin	2470 (1.0)	1110 (1.0)	0 (1.0)
omega prime preprochymosin	7280 (3.0)	10010 (9.1)	2180 ( )
In an analogous manner to the methods described above, various chimaeric RNA constructs were prepared with the NPT II coding region, and either omega prime, two tandem omega prime regions, a long (77 base) "junk" leader (polylinker) sequence or "junk" together with a central omega prime. The constructions are shown in Figure 17 and the results in Table 8 below:			

Table 8

EFFECT OF VARIOUS 5'-LEADER CONSTRUCTIONS ON IN VITRO  
TRANSLATION OF SP6 TRANSCRIPTS OF NEOMYCIN PHOSPHOTRANSFERASE

Cell-free Translation System

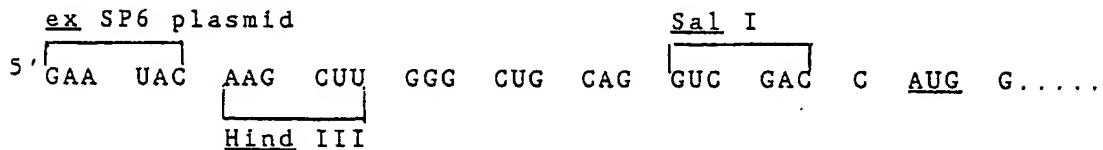
	Wheat Germ	Rabbit reticul-			<u>E.coli</u>	
		ocyte lysate	(-cap)	(+cap)	(-cap)	(+cap)
NPTII	1*	1	1	1	1	1
omega prime NPTII	8.1+	5.9	1.3	0.8	15.2	4.8
[omega-omega]prime NPTII		8.2	6.3	1.1	0.7	44.9 15.0
"JUNK"-NPTII	0.9	0.4	0.1	0.1	3.5	2.3
"JUNK"-omega prime NPTII		1.8	1.1	0.3	0.3	9.8 8.2

\*Background ( $H_2O$  or linearized DNA) corrected / All values = Fold-stimulation over NPTII RNA alone.

This shows that a random polylinker sequence will not substitute for omega prime in 80S ribosome systems and only poorly in a prokaryotic (70S) system. Also two tandem omega

primers only benefits 70S expression (c.f. single copy of omega prime).

To extend the data presented in Table 6 (ab ve) on the effect of omega prime on expression of the  $\beta$ -glucuronidase mRNA (GUS mRNA), a new series of constructs utilized the GUS gene with a modified sequence context around the initiation codon (AUG). Plasmid pRAJ275 , containing the "good context" leader



was the source for this version of GUS. Omega prime and various other leader constructs were inserted at the Hind III/Sal I sites as before. Details of the pRAJ275 construct are as follows:

pRAJ275 is a derivative of pRAJ255 (Jefferson. et al. Proc. Natl. Acad. Sci. 83, 8447 (1986)) in which the 5' sequences of GUS were removed by progressive BAL31 deletion and replaced with a synthetic oligonucleotide that has constructed a "consensus" translational initiator as defined by Kozak (Microbiol. Reviews, 47, 1 (1983)). This plasmid has a unique Nco I site (CCATGG) positioned at the initiator ATG codon, with the surrounding context GTCGACCATGGTC. It has been shown both in vitro and in vivo that the context around the initiator can have a profound effect on the levels of translated product from a given amount of mRNA. This

construction has been adjusted to maximise this effect. It was provided as a Sal I-Eco RI fragment in pUC19.

5'-capped or uncapped transcripts were electroporated into tobacco protoplasts as before and the level of GUS expression measured in extracts.

Uncapped RNAs were also added to MDL or WG cell-free translation systems and the level of GUS protein synthesized measured by excising and counting radioactive gel bands as for Figures 2, 3 etc. (Table 1). The results are shown in Table 9.

Table 9Translational Enhancement by omega prime on GUS mRNAIn vivo translationElectroporated tobacco protoplasts

	<u>In vitro translation</u>				
	Kozak context	Gus activity nmoles 4-methyl umbelliferyl glucuronide cleaved min <sup>-1</sup> /μg protein in protoplast extract	Fold stimulation	Cpm 35S methionine-labelled GUS in gel bands	MDL
Uncapped RNAs					
GUS 235 (40b poly-linker leader)	bad	<0.01	(1)	7180	(1.0)
Omega prime-235	bad	0.18	(>18)	19700	(2.7)
GUS 275 (28b poly-linker leader)	good	<0.01	(1)	12920	(1.0)
Omega prime-275	good	0.35	(>35)	29280	(2.3)
				19720	(1.0)
				19720	(6.6)

Fold stimulation  
Cpm 35S methionine-labelled GUS in gel bands

35

Cont/d....

Table 9 cont/d.....

Translational Enhancement by omega prime on GUS mRNAIn vivo translationElectroporated tobacco protoplasts

Kozak context	Gus activity nmoles 4-methyl umbelliferyl glucuronide cleaved min <sup>-1</sup> /μg protein in protoplast extract	Fold stimulation
5'capped leader	0.03	(1)
GUS 235 (40b poly-linker leader)	bad	0.61 (20)
Omega prime-235	bad	0.04 (1)
GUS 275 (28b poly-linker leader)	good	3.2 (80)
Omega prime-275	good	

Again in all cases, both in vitro (MDL,WG) and in vivo (protoplasts) with 5' capped or uncapped GUS mRNAs, with good or bad Kozak context around the initiation codon, omega prime enhances mRNA expression significantly.

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A further set of RNA constructs was prepared, in an analogous manner to the method described above, with the E. coli reporter gene  $\beta$ -glucuronidase (GUS) and additionally the inducible tryptophan (Trp) promoter. The Trp promoter was purchased from Pharmacia Ltd., and modified by conventional techniques of restriction endonuclease digestion, filling-in, sub-cloning etc, to create a 3'-Hind III site (Fig. 18) and a blunt 5'-end. This dsDNA fragment was then inserted into the various leader-reporter (GUS) gene plasmids between the SP6 promoter (silent in E. coli in vivo) and the 5'-leader construct of interest.

The resulting plasmid DNA was used to transform competent E. coli cells by standard techniques and the Trp promoter induced in situ to produce chimaeric leader-reporter mRNAs. Transcription start point corresponds to the G in the Hind III site (AAGCTT).

Expression of the transcripts in transformed E. coli cells was determined spectrophotometrically (Jefferson et al. Proc. Natl. Acad. Sci. 83 8447 (1986)). Results (Table 10) indicate that expression of GUS was enhanced in vivo from either the "good" or "bad" Kozak context construct by the presence of omega prime and to some extent by the other leader sequences or derivatives of omega prime.

Table 10

Expression controlled by the Trp promoter in stably transformed E. coli cells

Approximate relative spectro-  
photometric rates of conversion of  
p-nitrophenyl glucuronide

235-GUS ("Bad" context)	1
omega prime 235 GUS	7x
275-GUS ("Good" context)	1
omega prime-275-GUS ("Good" context)	8x
$\Delta 1$ -275-GUS	5 - 8x
$\Delta 2$ 275 GUS	(75x : To be confirmed)
$\Delta 3$ 275 GUS	(75x : To be confirmed)
$\Delta 4$ 275 GUS	5 - 8x
$\Delta 5$ 275 GUS	5 - 8x
A $\rightarrow$ C 275 GUS	(75x : To be confirmed)
[C,A] <sub>n</sub> $\rightarrow$ [U] <sub>n</sub> 275 GUS	5x
TYMV 275 GUS	3 - 4x
AlMV4 275 GUS	3 - 4x
BMV3 275 GUS	1 - 2x
RSV 275 GUS	1 - 2x

(The results above were normalized to the respective GUS construct with the polylinker leader alone.

Conclusions:

Omega prime enhances the expression of GUS RNA in vivo in E. coli transformed with plasmid DNAs, using Trp promoter in situ.

Further experiments were performed using supercoiled double stranded pUC19 DNA which is modified to contain the cauliflower mosaic virus (CaMV) 35S promoter, the nopaline synthase terminator (from Agrobacterium tumefaciens) and in between them either CAT DNA ( $\theta, \Delta$ ) or omega prime CAT DNA ( $\theta, \Delta$ ).

The constructs (Figure 20) were prepared from a binary vector system (Bevan, Nuc Acids Res. 12 8711 (1984)) wherein the CaMV 35S promoter and the Nos terminator were excised using Hind III and Eco RI sites and inserted into plasmid pUC19 thus giving pUC35S Nos.

The constructs pUC35SCATNos and pUC35S omega prime CATNos were made by inserting either CAT or omega prime CAT respectively into the plasmids using the Bam HI site.

Various levels of either plasmid DNA (in  $\mu\text{g}/\text{ml}$ ) were electroporated into protoplasts as before, and the cells incubated at  $25^\circ\text{C}$  for 6hours ( $0,0$ ) or 26hours ( $\Delta,\Delta$ ) and lysed. CAT assays (as before) were carried out.

The results as seen in Figure 20 indicate that cells which received  $100\mu\text{g} - 150\mu\text{g}$  of supercoiled plasmid DNA showed enhanced CAT expression (2 fold) when omega prime is present in the construct ( $\Delta,0$ ).

These results show that gene expression in stable transgenic plants will also likely be enhanced by the inclusion of the omega prim sequence between the promoter (for transcription in vivo) and the translational open reading frame.

CLAIMS

1. Use of the 5'-leader sequence of an RNA virus up to the first initiation codon of the viral RNA (or a derivative or portion thereof), either as RNA or as complementary DNA, as an enhancer of translation of mRNA when the 5'-leader is contiguous with the mRNA.
2. Use according to claim 1, in which the RNA virus is a plant virus.
3. Use according to claim 2, in which the plant virus is tobacco mosaic virus.
4. Use according to claim 3, in which the 5'-leader sequence is omega prime as herein defined, or a derivative or portion thereof.
5. Use according to any of claims 1 to 4, in which the 5'-leader sequence includes a 5'-cap.
6. mRNA including the 5'-leader sequence as defined in any of claims 1 to 5, and downstream sequence not derived from the virus providing the leader sequence.
7. A DNA sequence complementary to the 5'-leader sequence

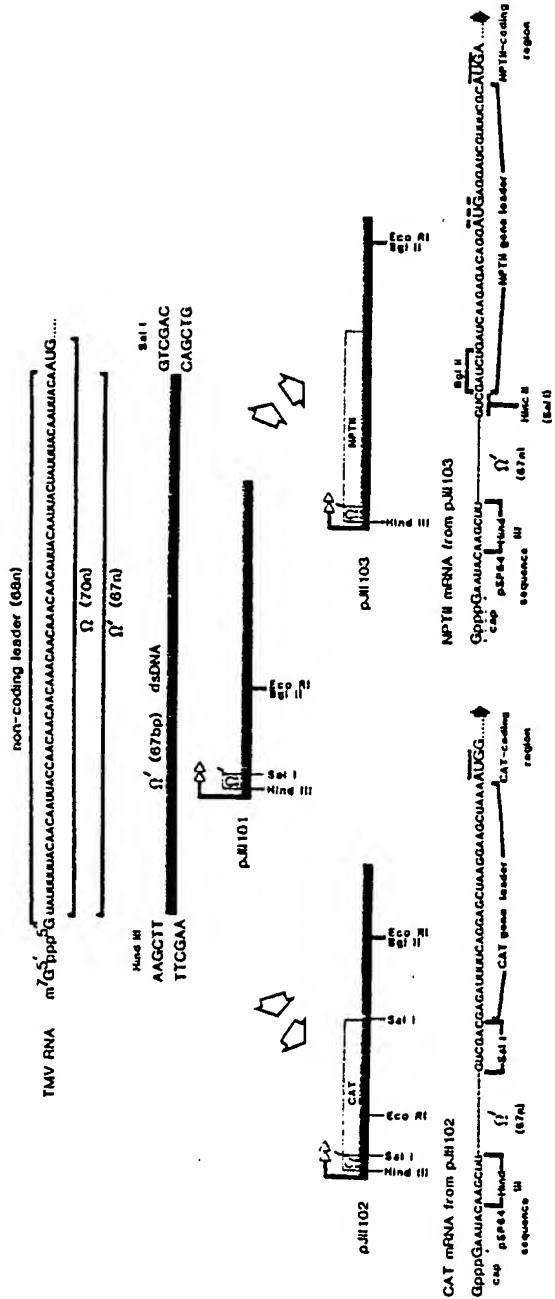
as defined in any of claims 1 to 4.

8. A DNA sequence comprising a promoter, a sequence complementary to the 5'- leader sequence as defined in any of claims 1 to 4, and an open reading frame including an appropriate initiation codon.

9. A DNA sequence according to claim 8, including sequence used to enhance transcription.

10. An expression vector including a DNA sequence according to claim 8 or 9.

11. A living organism having incorporated in its cells a DNA sequence according to claim 8 or 9, whereby expression of the protein coded by the open reading frame is enhanced.



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M, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11      12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22  
kDa  
69-

46-



Fig. 2

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M, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11  
kDa  
69-

46-

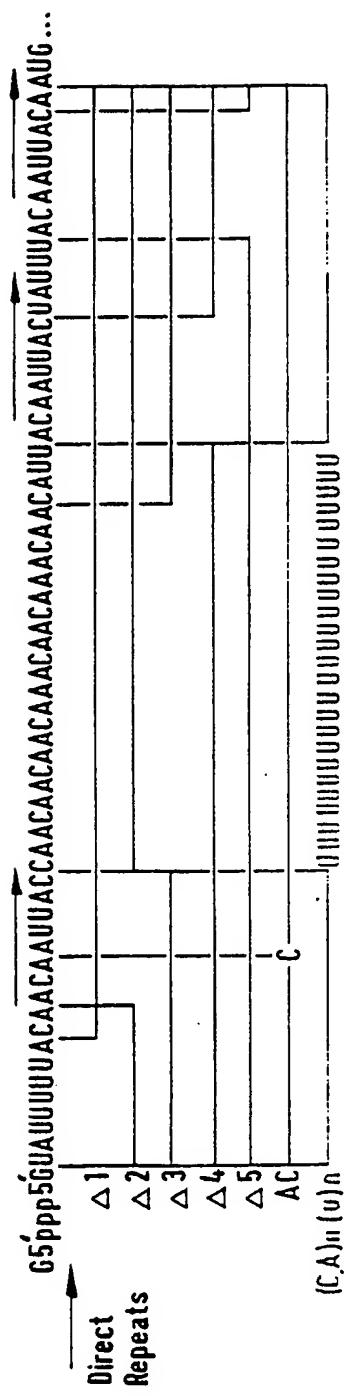
30-



Fig.3

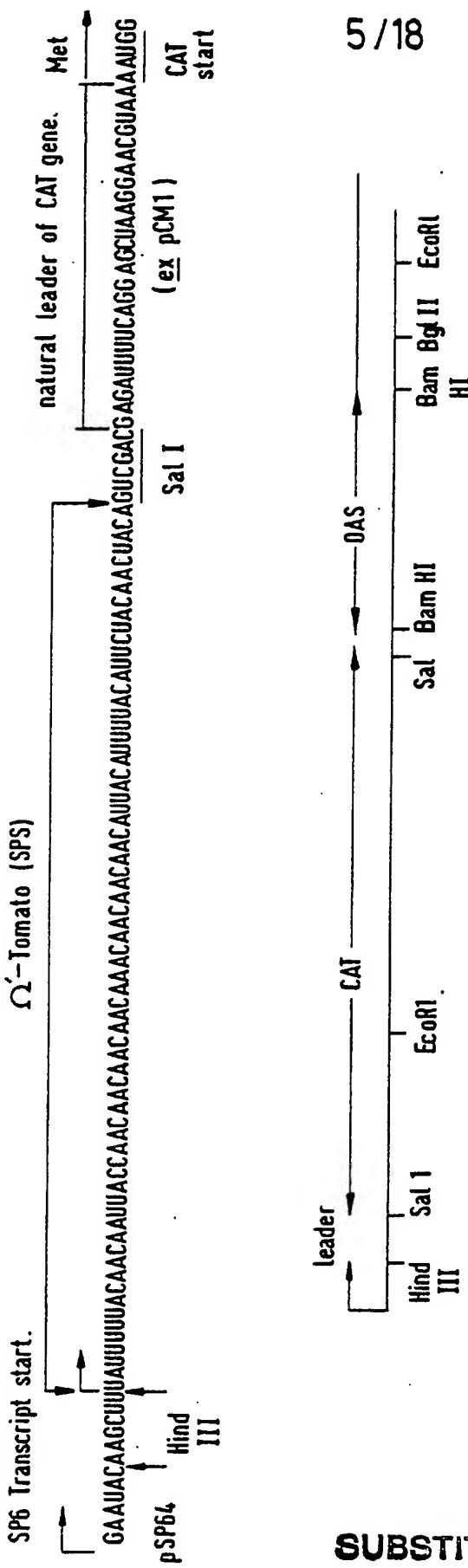
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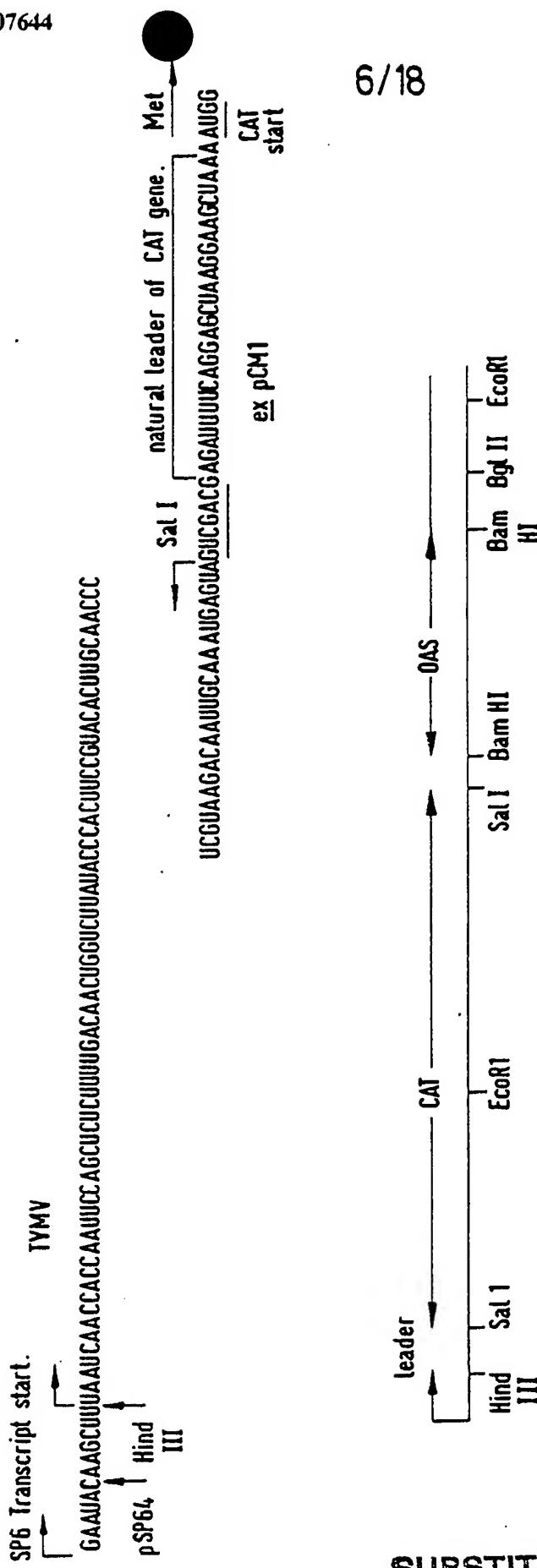


fig

Name : p JII 168

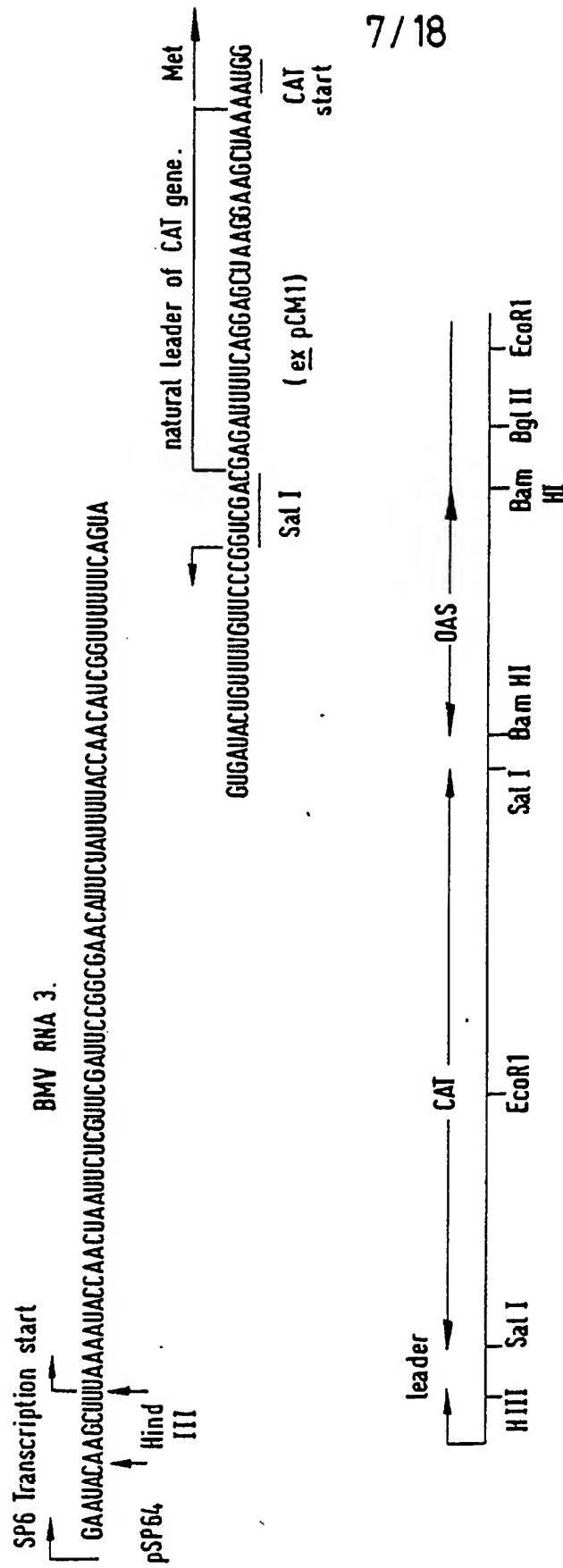
Leader: Omega-tomato

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**Fig. 6**

Name : p JII169  
 Leader : T7MV

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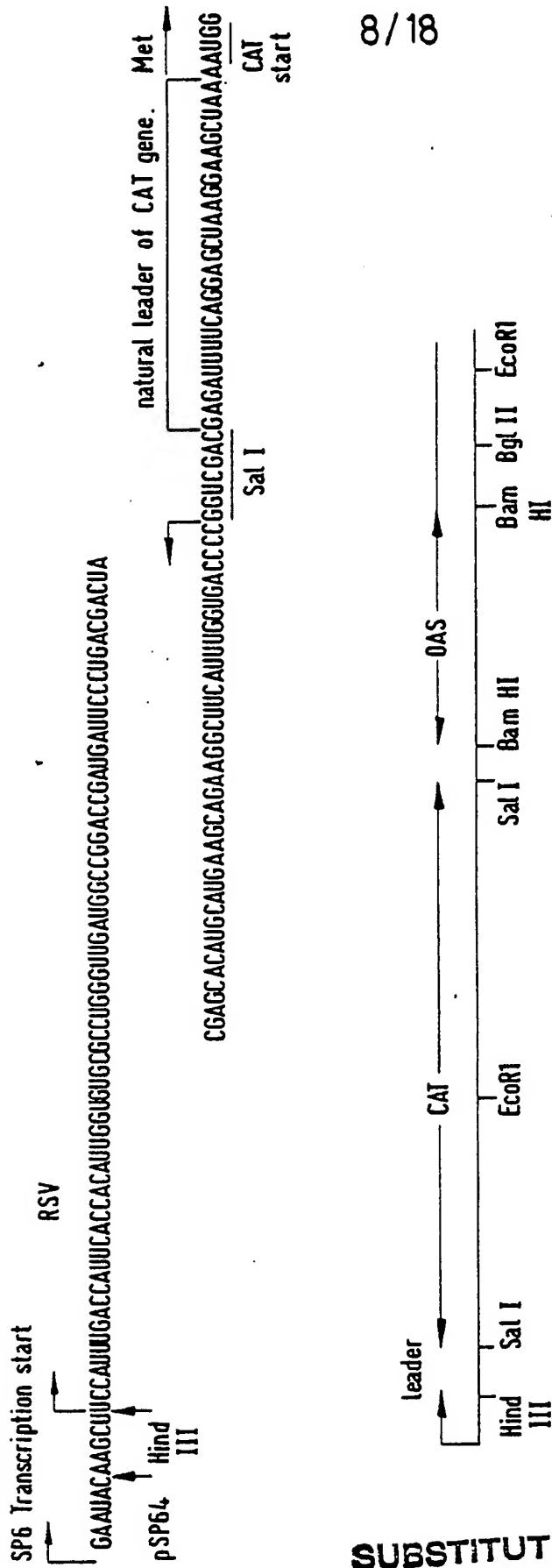
**Fig. 7**

Name : pJII170

Leader : BMV RNA3

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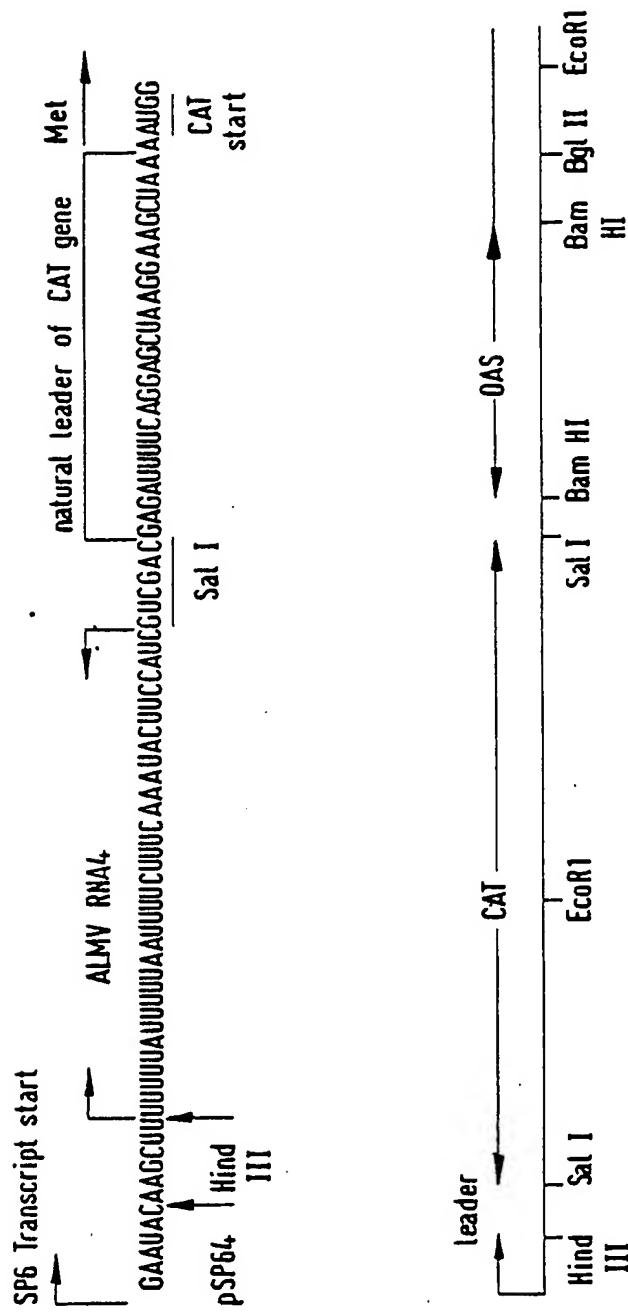
**Fig. 8**

Name : pIII171

Leader: RSV

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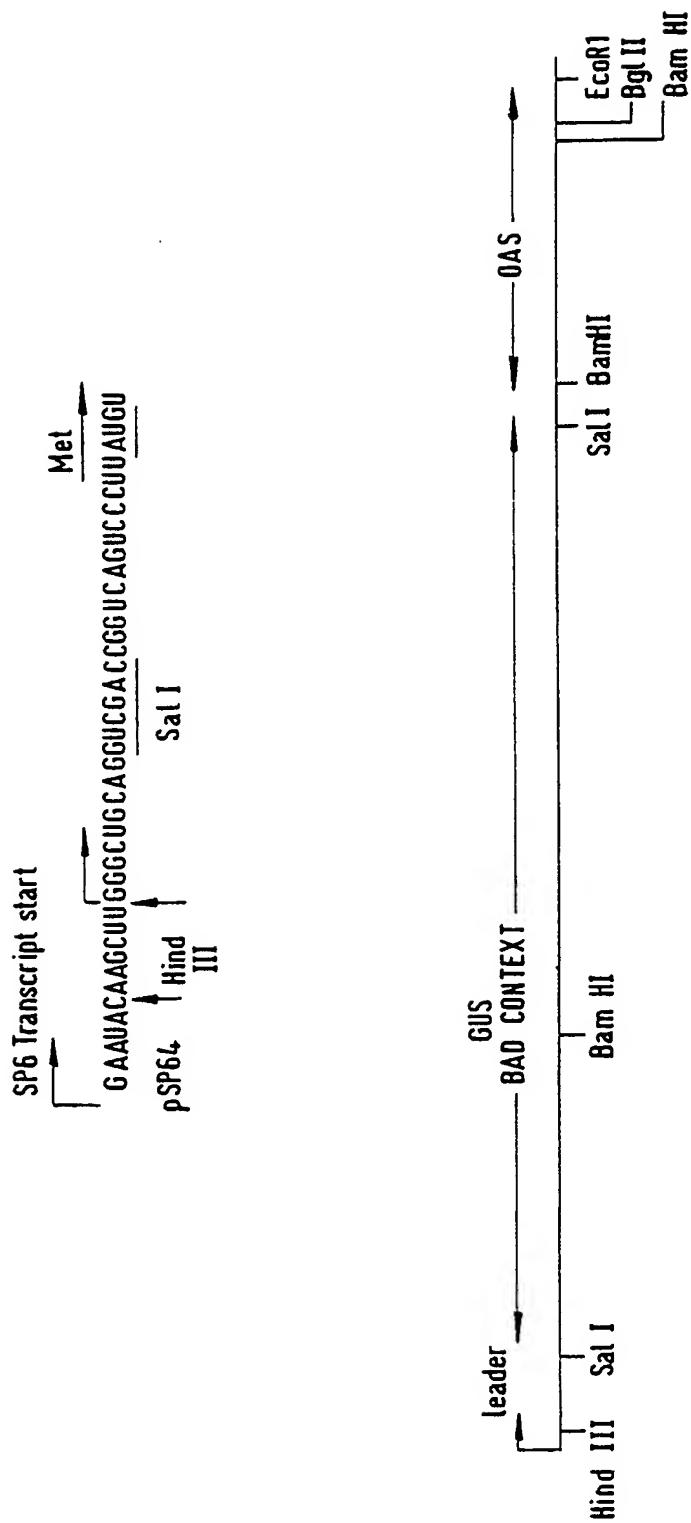
**Fig. 9**

Name : pJII172

Leader : ALMV RNA4

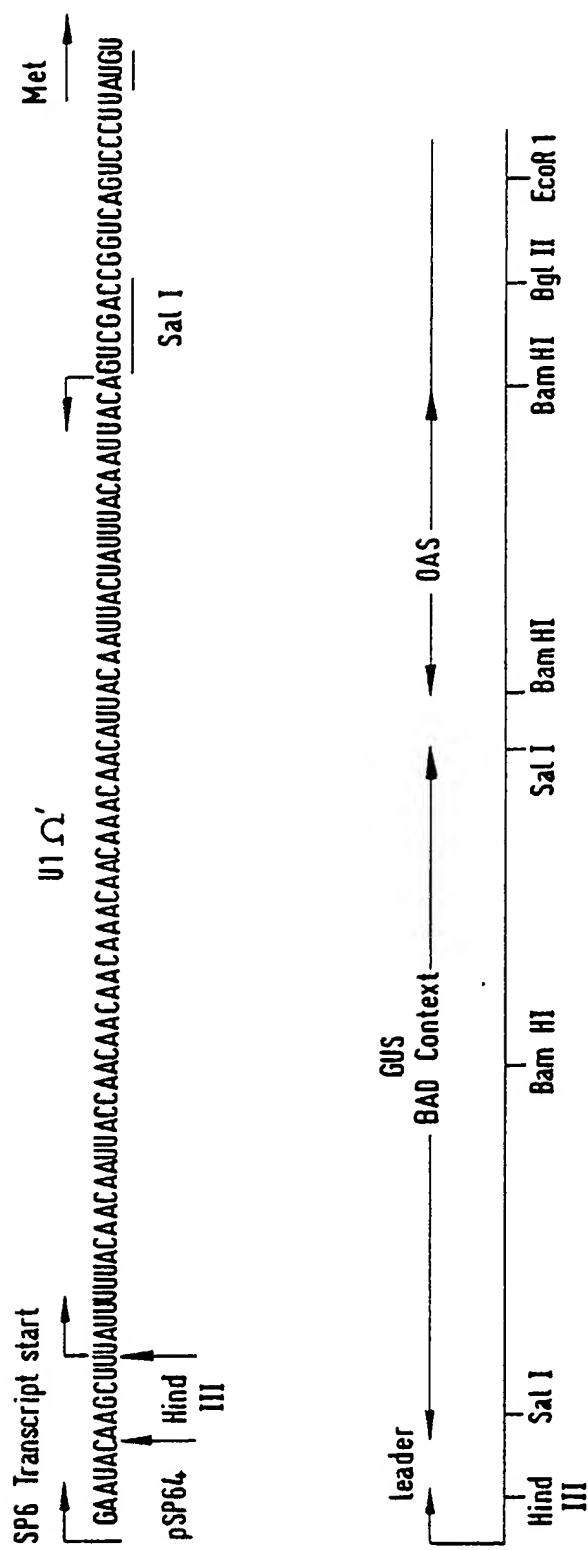
**SUBSTITUTE SHEET**

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**Fig. 10**

Name : pII1119  
 Leader : polylinker

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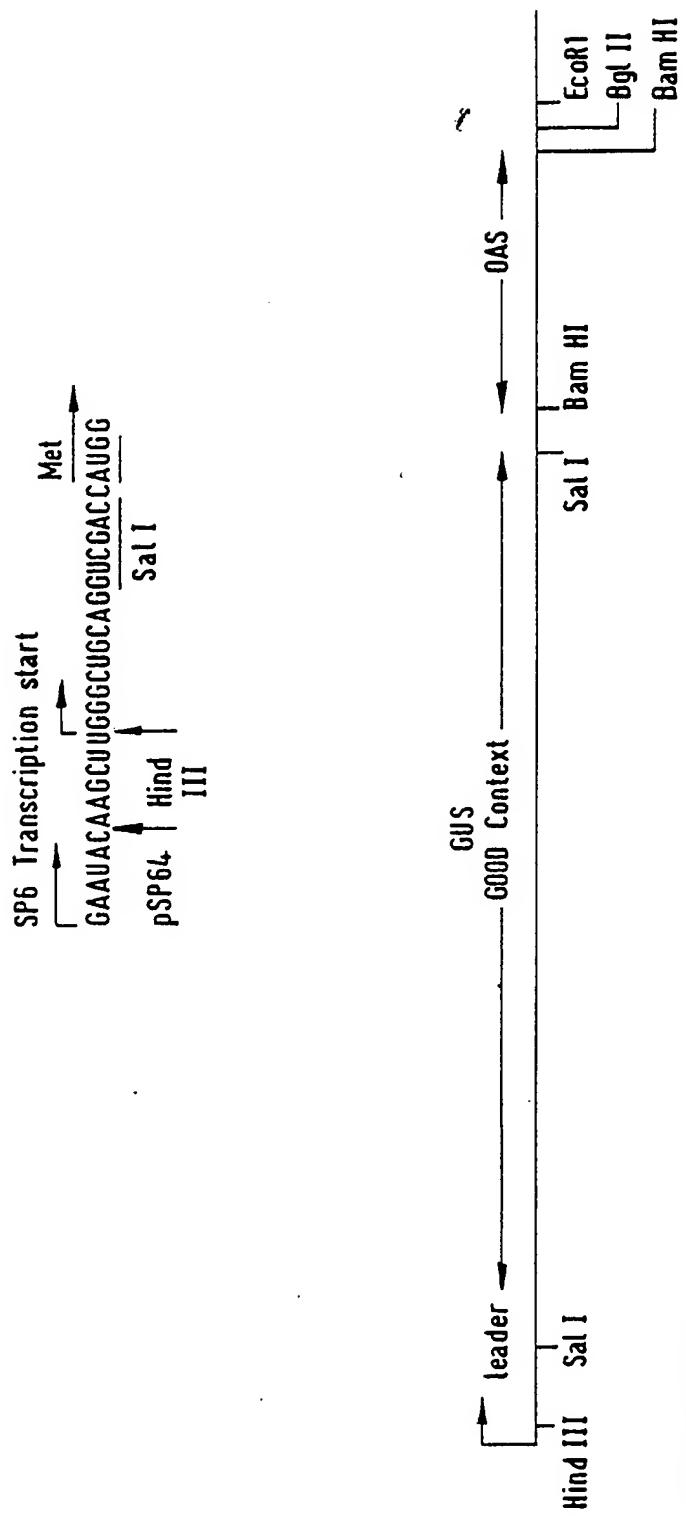


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Name: pJII120  
Leader: U1 - Q

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**Fig. 12**

Name : pJII139  
 Leader : polylinker

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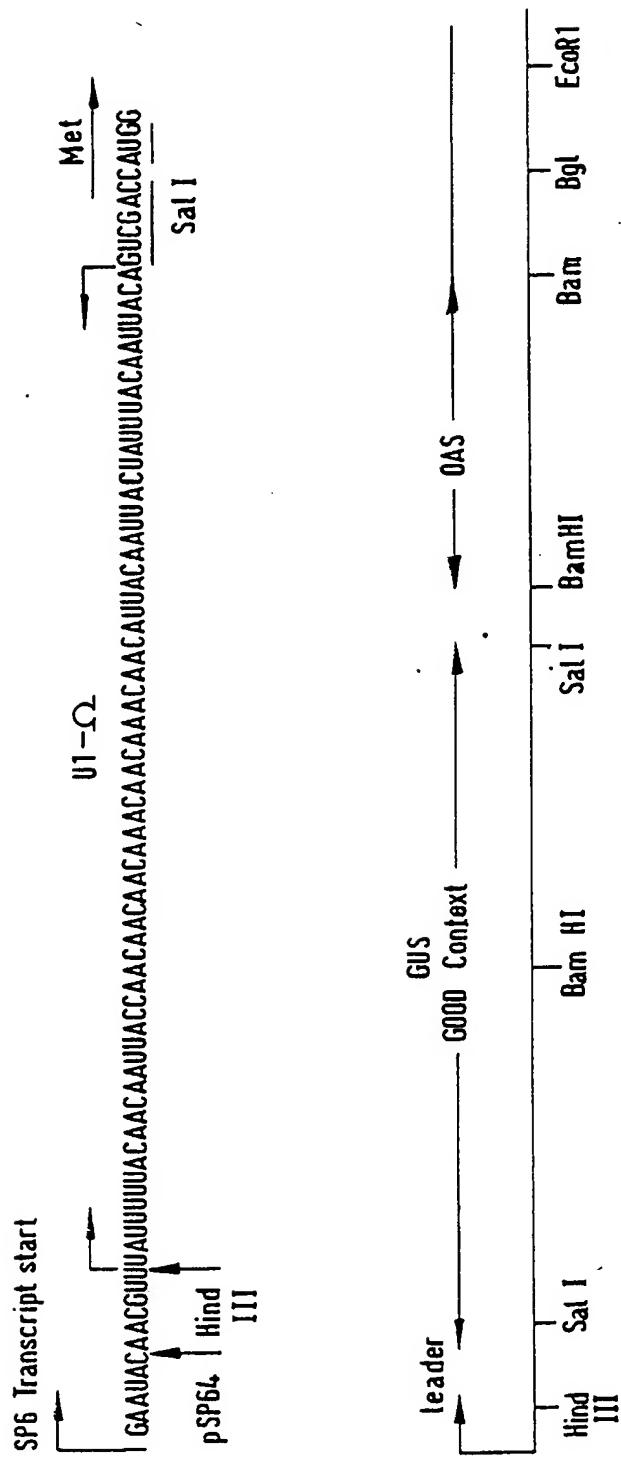


Fig. 13

Name : pJ114.0  
 Leader :  $\text{U1}-\Omega$

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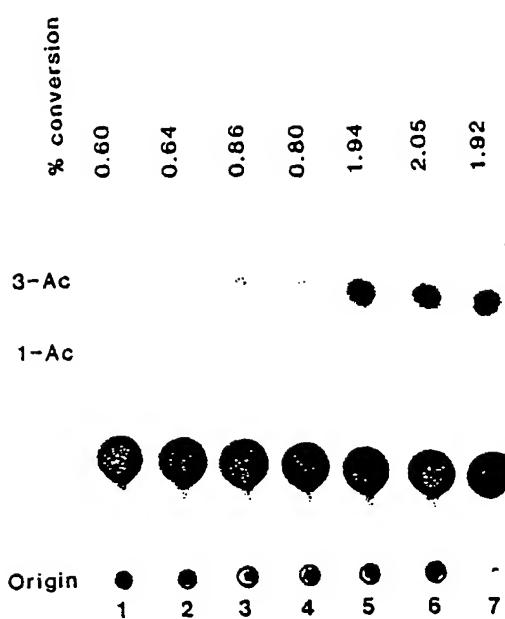


Fig. 14

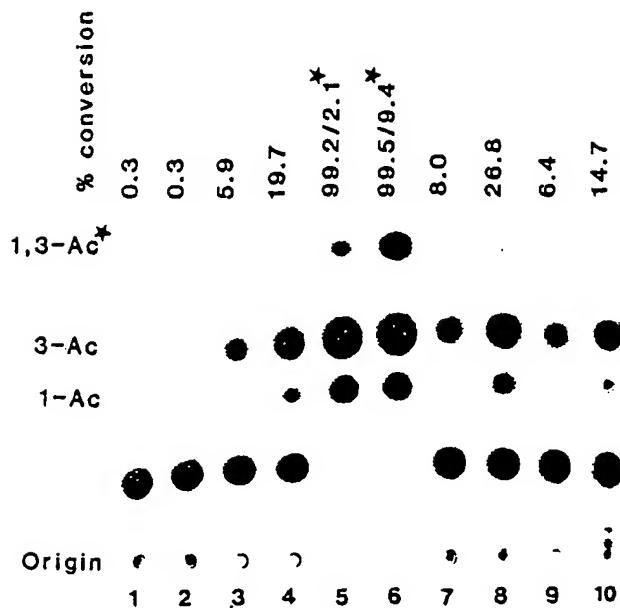
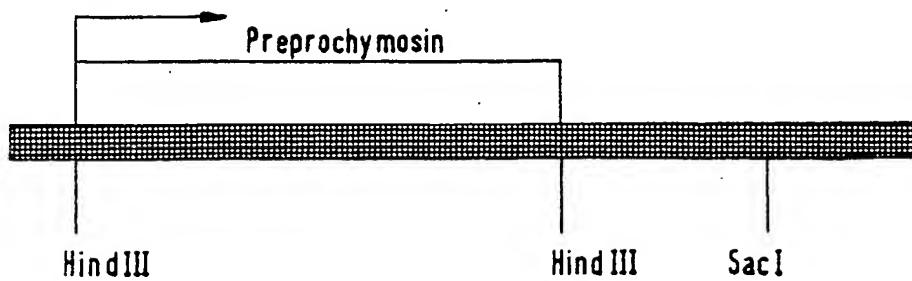


Fig. 15

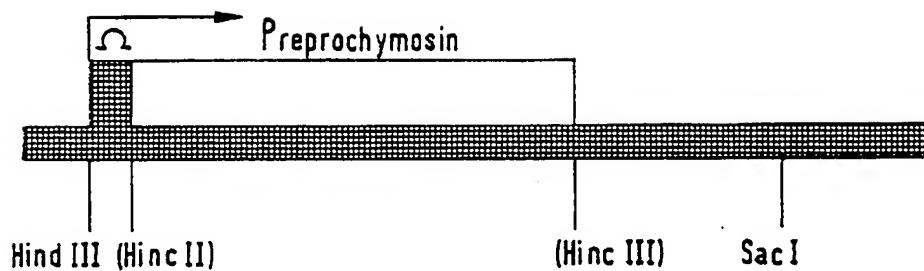
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pSP64CT

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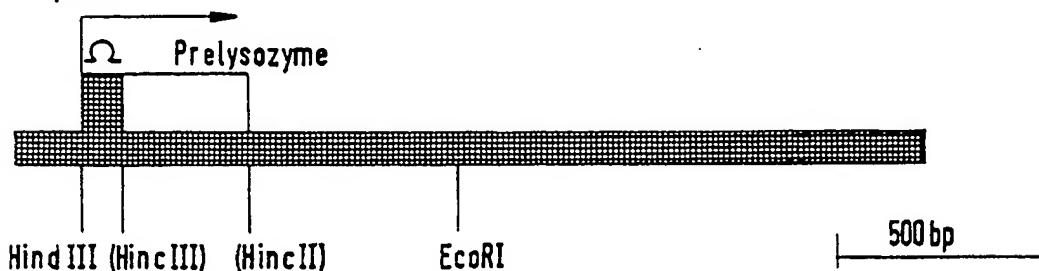
pJ116



pSP64LT



pJ117



500 bp

Fig. 16  
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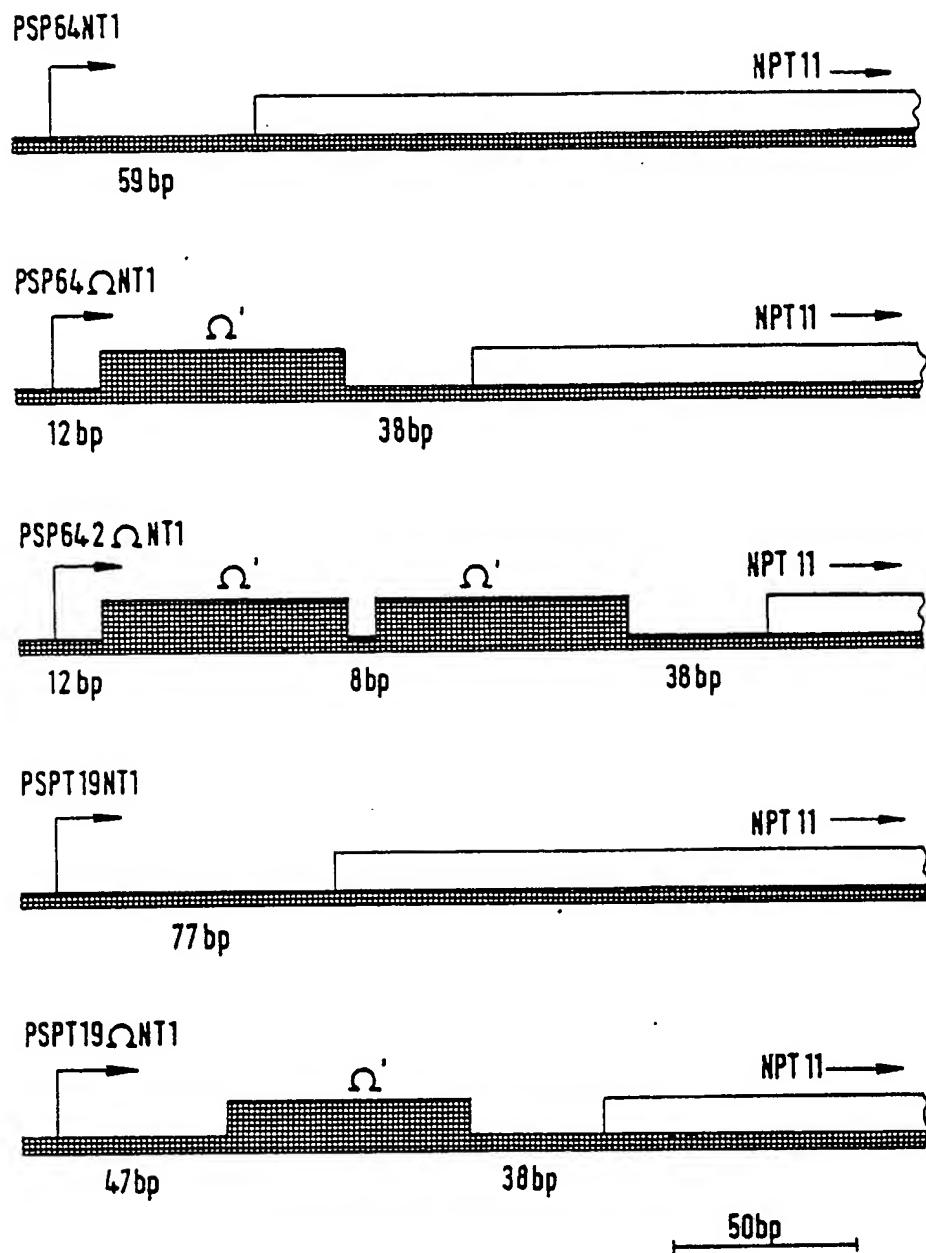
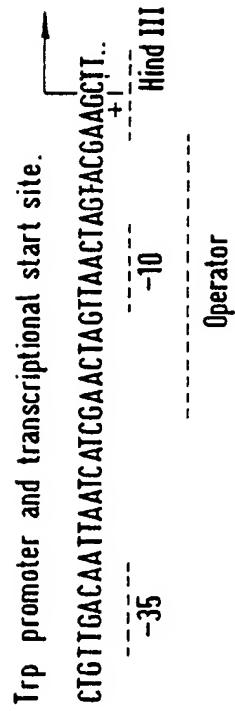
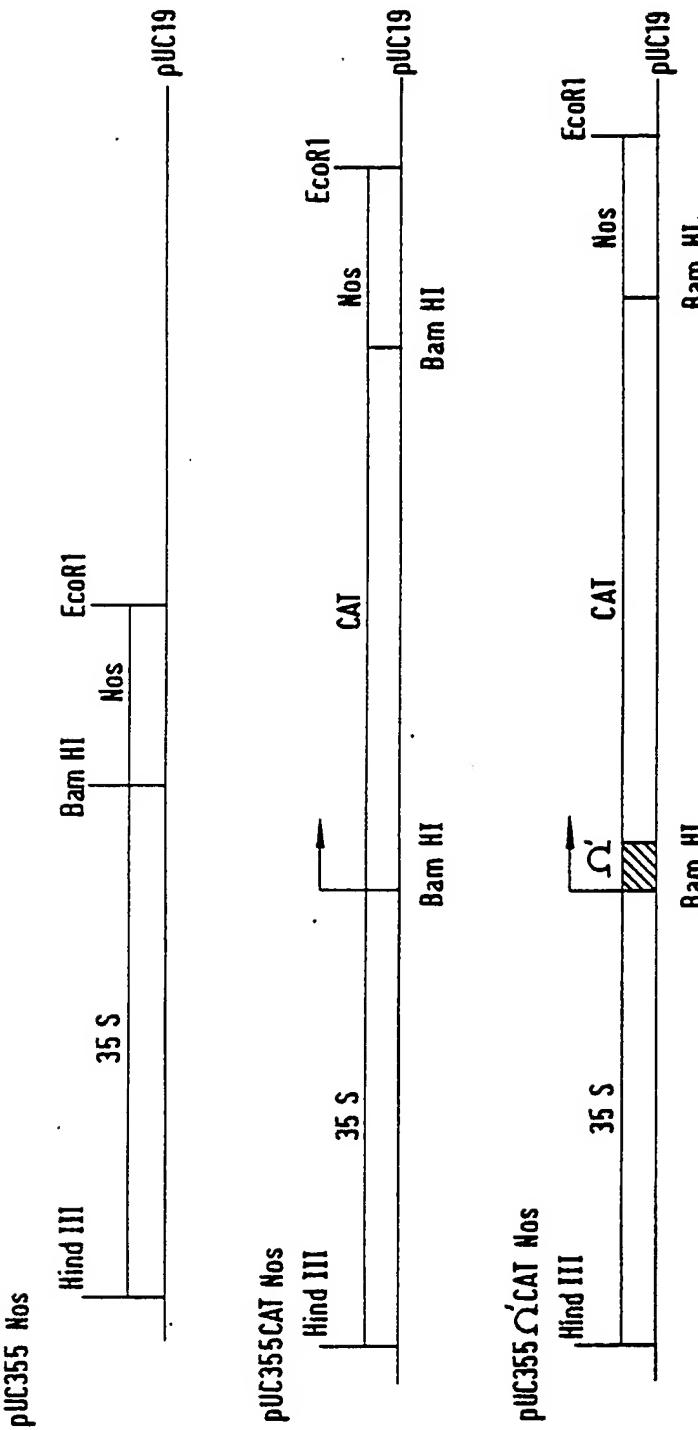


Fig. 17

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**Fig. 18****Fig. 19****SUBSTITUTE SHEET**

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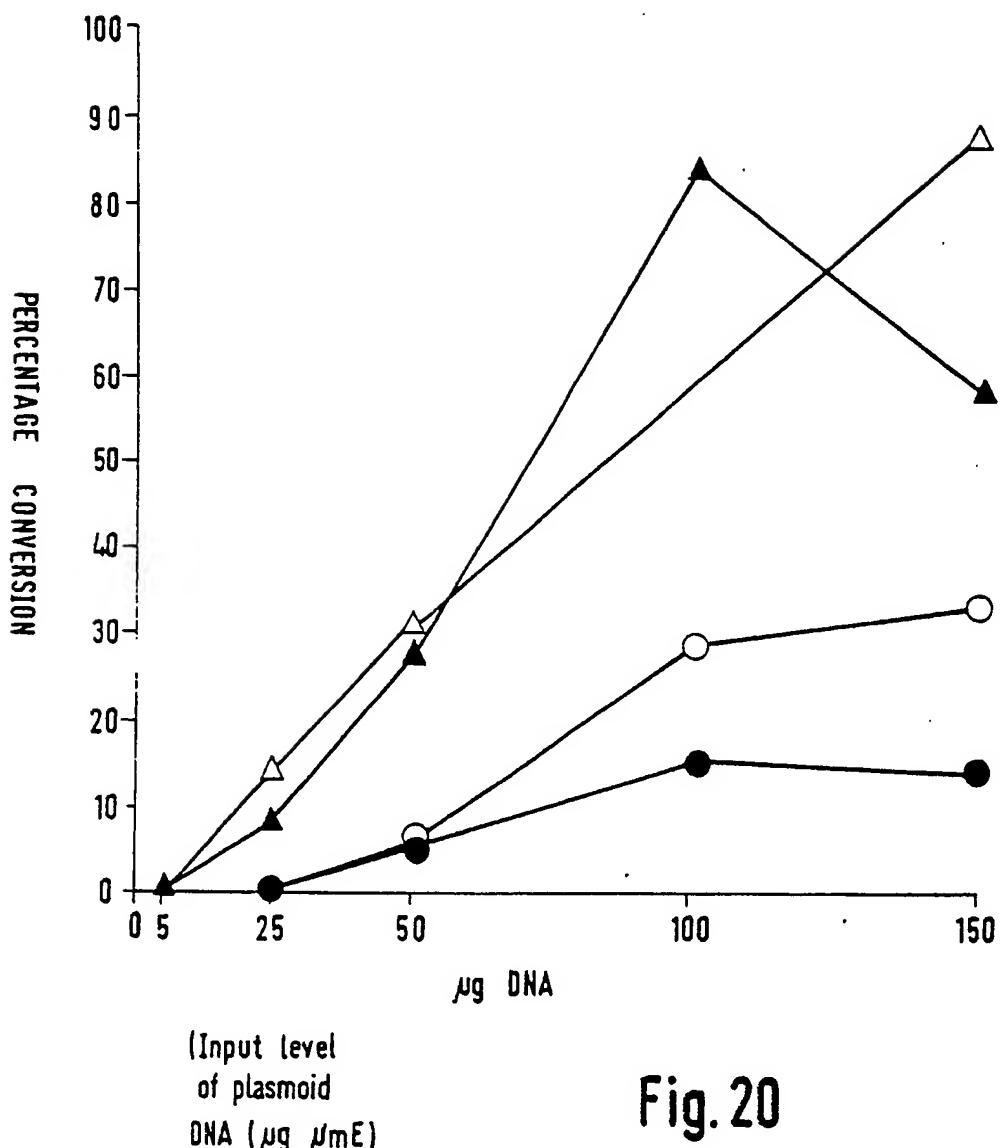


Fig. 20

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# INTERNATIONAL SEARCH REPORT

International Application No PCT/GB 87/00390

## I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC<sup>4</sup> : C 12 N 15/00

## II. FIELDS SEARCHED

Classification System	Minimum Documentation Searched <sup>7</sup>	
	Classification Symbols	
IPC <sup>4</sup>	C 12 N	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched <sup>8</sup>		

## III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup>

Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
X	Science, vol. 231, 14 March 1986 R. French et al.: "Bacterial gene inserted in an engineered RNA virus: efficient expression in monocotyledonous plant cells", pages 1294-1297, see the whole document	1,2,6,7,8,10 11
X	Chemical Abstracts, vol. 103, 1985 (Columbus, Ohio, US) L. Sue Loesch-Fries et al.: "Expression of alfalfa mosaic virus RNA 4 cDNA transcripts in vitro and in vivo", see abstract no. 190686, & Virology 1985, 146(2), 177-87 (Eng)	1,2,5,7,8, 10,11
X	Proc. Natl. Acad. Sci., vol. 83, March 1986, Genetics (US) W.O. Dawson et al.: "cDNA cloning of the complete genome of tobacco mosaic virus and production of infectious transcripts", pages 1832-1836, see the whole document	1-5,7,8,10, 11 . /.

\* Special categories of cited documents: 10

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"A" document member of the same patent family

## IV. CERTIFICATION

Date of the Actual Completion of the International Search  
21st August 1987

Date of Mailing of this International Search Report

- 8 OCT 1987

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

M VAN MOL

## III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
X	EP, A, 0067553 (NATIONAL RESEARCH COUNCIL OF CANADA) 22 December 1982 see page 15, lines 1-18; page 18, lines 1-14; page 23, lines 6-15; page 27, line 13 - last line; page 31, lines 10-25 --	1-5,7,8
P, X	Nucleic Acids Research, vol. 15, no. 8, 24 April 1987 D.R. Gallie et al.: "The 5'-leader sequence of tobacco mosaic virus RNA enhances the expression of foreign gene transcripts in vitro and in vivo", pages 3257-3273, see the whole document --	1-11
P, X	EP, A, 0194809 (LUBRIZOL GENETICS) 17 September 1986 see example 4 --	1,2,6-8,10, 11
X	Proc. Natl. Acad. Sci. (USA), vol. 79, October 1982, Biochemistry P. Goelet et al.: "Nucleotide sequence of tobacco mosaic virus RNA", pages 5818-5822, see the whole document --	7
P, X	Biological Abstracts, Biosciences Information Service, vol. 82, no. 5, 1986 (Philadelphia, PA, US) L. Gehrke: "Preparation of messenger RNA transcripts for secondary structure analysis using SP6 polymerase, guanylyltransferase and preparative gel electrophoresis" see abstract no. 40900, & Gene Anal. Tech, 3(3):45-52, 1986 --	1,2,5,6
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## III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
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## ANNEX TO THE INTERNATIONAL SEARCH REPORT

INTERNATIONAL APPLICATION NO.

PCT/GB 87/00390 (SA 17422)

This Annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on 21/09/87

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